



IFW16

RAW SEQUENCE LISTING

DATE: 08/27/2004

PATENT APPLICATION: US/09/390,846

TIME: 10:15:26

Input Set : N:\Cr3\RULE60\09390846.raw

Output Set: N:\CRF4\08272004\I390846.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Kok, Jacobus Johannes

7 van den Boogaart, Paul

8 Vermeulen, Arnoldus Nicolaas

11 (ii) TITLE OF INVENTION: Coccidiosis poultry vaccine

14 (iii) NUMBER OF SEQUENCES: 2

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Akzo Nobel Patent Department

19 (B) STREET: 1300 Piccard Drive, Suite 206

20 (C) CITY: Rockville

21 (D) STATE: Maryland

22 (E) COUNTRY: USA

23 (F) ZIP: 20850

26 (v) COMPUTER READABLE FORM:

27 (A) MEDIUM TYPE: Floppy disk

28 (B) COMPUTER: IBM PC compatible

29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

33 (vi) CURRENT APPLICATION DATA:

C--> 34 (A) APPLICATION NUMBER: US/09/390,846

C--> 35 (B) FILING DATE: 14-Sep-1999

36 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: US/08/676,882

40 (B) FILING DATE: 03-JUL-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Gormley, Mary E.

44 (B) REGISTRATION NUMBER: 34,409

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: (301) 258-5200

49 (B) TELEFAX: (301) 977-0847

52 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

56 (A) LENGTH: 1679 base pairs

57 (B) TYPE: nucleic acid

58 (C) STRANDEDNESS: double

59 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: cDNA to mRNA

65 (iii) HYPOTHETICAL: NO

68 (iv) ANTI-SENSE: NO

71 (vi) ORIGINAL SOURCE:

72 (A) ORGANISM: Eimeria acervulina



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73          (D) DEVELOPMENTAL STAGE: Schizont
76      (vii) IMMEDIATE SOURCE:
77          (B) CLONE: EASC2_1
80      (ix) FEATURE:
81          (A) NAME/KEY: CDS
82          (B) LOCATION:280..1269
83          (D) OTHER INFORMATION:/function= "Eimeria lactate
84 dehydrogenase"
87      (ix) FEATURE:
88          (A) NAME/KEY: misc_feature
89          (B) LOCATION:1..51
90          (D) OTHER INFORMATION:/label= pBluescriptII
93      (ix) FEATURE:
94          (A) NAME/KEY: misc_feature
95          (B) LOCATION:1624..1679
96          (D) OTHER INFORMATION:/label= pBluescriptII
99      (ix) FEATURE:
100          (A) NAME/KEY: misc_feature
101          (B) LOCATION:45..54
102          (D) OTHER INFORMATION:/label= EcoRI-linker
105      (ix) FEATURE:
106          (A) NAME/KEY: misc_feature
107          (B) LOCATION:1621..1630
108          (D) OTHER INFORMATION:/label= EcoRI-linker
112      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
114 GCGGTGGCGG CCGCTCTAGA ACTAGTGGAT CCCCCGGGCT GCAGGAATTC GGGTTTTTTTT      60
117 TTTTTTTTCT ACACATTAAT ATTCTTCGTT TACGTTTATT TTGCTACAAA TAAACCCCTT      120
120 AAACCTCTCTA TTTCCTCATA TTCTACCGCT TCATCGGTGG GTGTGTAAGA CGTACGTACG      180
123 TACAGCTGGG GCTGGCTTAC TGCACACCGC TTATTTATTA CTTAATTCAT ACACATTTTA      240
126 TATCTTTCTT CTTCTTTTTT CTTGCTCTTT CTTGTGAAA ATG GCG GTC TTC GAG      294
127                                     Met Ala Val Phe Glu
128                                     1      5
131 AAG AAT ACA CGC CCC AAG ATT GCT ATG GTG GGC TCC GGT ATG ATT GGA      342
132 Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly Ser Gly Met Ile Gly
133          10          15          20
136 GGC ACC ATG GCT TTC CTG TGC AGC TTG AGG GAA CTC GGA GAT GTT GTC      390
137 Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu Leu Gly Asp Val Val
138          25          30          35
141 CTC TTC GAC GTT GTA CCG AAC ATG CCG ATG GGG AAG GCG ATG GAT ATA      438
142 Leu Phe Asp Val Val Pro Asn Met Pro Met Gly Lys Ala Met Asp Ile
143          40          45          50
146 TCG CAC AAT TCG TCG GTG GTT GAC ACG GGT ATA ACA GTA TAC GGC TCA      486
147 Ser His Asn Ser Ser Val Val Asp Thr Gly Ile Thr Val Tyr Gly Ser
148          55          60          65
151 AAT TCA TAC GAG TGC TTG AAG GGT GCG GAC GTA GTA ATA ATA ACA GCA      534
152 Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val Val Ile Ile Thr Ala
153          70          75          80          85
156 GGG ATA ACA AAG ATA CCC GGA AAG AGC GAT AAA GAA TGG TCT AGA ATG      582
157 Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys Glu Trp Ser Arg Met

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158		90		95		100	
161	GAT CTA TTA CCT GTG AAT ATA AAG ATA ATG AGG GAG GTC GGT GCA GCA						630
162	Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg Glu Val Gly Ala Ala						
163		105		110		115	
166	ATT AAA TCT TAC TGT CCT AAT GCA TTT GTT ATT AAT ATA ACA AAT CCT						678
167	Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile Asn Ile Thr Asn Pro						
168		120		125		130	
171	TTA GAT GTG ATG GTA GCT GCT CTT CAA GAG TCA TCA GGA CTA CCT CAT						726
172	Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser Ser Gly Leu Pro His						
173		135		140		145	
176	CAT AGA ATC TGC GGT ATG GCT GGG ATG CTT GAT AGC TCT CGT TTT AGA						774
177	His Arg Ile Cys Gly Met Ala Gly Met Leu Asp Ser Ser Arg Phe Arg						
178	150		155		160		165
181	CGT ATG ATA GCT GAT AAA TTA GAA GTC TCT CCT AGA GAT GTA CAG GGG						822
182	Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro Arg Asp Val Gln Gly						
183		170		175		180	
186	ATG GTC ATA GGT GTA CAC GGC GAT CAT ATG GTG CCC CTA AGT AGA TAT						870
187	Met Val Ile Gly Val His Gly Asp His Met Val Pro Leu Ser Arg Tyr						
188		185		190		195	
191	GCA ACA GTT AAC GGC ATC CCG CTT TCT GAG TTT GTT AAG AAG GGC TGG						918
192	Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe Val Lys Lys Gly Trp						
193		200		205		210	
196	ATC AAG CAA GAA GAA GTA GAT GAT ATC GTT CAG AAG ACC AAG GTC GCT						966
197	Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln Lys Thr Lys Val Ala						
198		215		220		225	
201	GGA GGA GAG ATC GTA CGC CTA TTA GGA CAA GGC TCT GCT TAC TAT GCT						1014
202	Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly Ser Ala Tyr Tyr Ala						
203	230		235		240		245
206	CCA GGG GCT TCA GCT ATT CAG ATG GCT GAG AGC TAT CTA AAG GAT AGA						1062
207	Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser Tyr Leu Lys Asp Arg						
208		250		255		260	
211	AAG AGA GTG ATG GTT TGC TCT TGC TAC TTG CAA GGA CAA TAT GGT GTA						1110
212	Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln Gly Gln Tyr Gly Val						
213		265		270		275	
216	CAG AAT CAC TAC TTA GGA GTA CCT TGT GTT ATC GGT GGG AGA GGT GTT						1158
217	Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile Gly Gly Arg Gly Val						
218		280		285		290	
221	GAG AAG ATT ATT GAG TTA GAA TTG ACC GCA CAA GAA AGA CAG GAG CTT						1206
222	Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln Glu Arg Gln Glu Leu						
223		295		300		305	
226	CAG GGA TCT ATC GAT GAG GTT AAG GAG ATG CAG AAG GCT ATT GCT GCT						1254
227	Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln Lys Ala Ile Ala Ala						
228	310		315		320		325
231	CTT GAT GCA TCC AAG TAAGCAGCAG CAAAATCGCA GAAGTTGCAG CGCTAGAACA						1309
232	Leu Asp Ala Ser Lys						
233		330					
236	ACCAGCAGCA GCAGCAGCAG CAGCCTATAG TTCTTGCTGC TGCTGTTCCCT ACTACAGCTG						1369
239	CGGCTTTCTT CCTCGTGTTA TTATCATGAT AGTAAGCTGC TGTACCAGCA GCAGCAGCAG						1429
242	CAGCAGATTT TGCTTGCACC GCCGTTTGTT TTGCGTACAC CGGCAGAAAT ATTGACTTGC						1489

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245 AGTTAGGAGA AAGAAAGAAA ACAAAACACGA TCCCATCGAT CCCAATAAAC CCCACACTGT      1549
248 CGATCCCATC GATCCCAGCA ACTCCACGGG GCTCTTAACT GTTAAACCTA TTATTCTTAT      1609
251 CATTACTGTC TCCCGAATTC GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGG      1669
254 CCGGTACCCA                                     1679
257 (2) INFORMATION FOR SEQ ID NO: 2:
260     (i) SEQUENCE CHARACTERISTICS:
261         (A) LENGTH: 330 amino acids
262         (B) TYPE: amino acid
263         (D) TOPOLOGY: linear
267     (ii) MOLECULE TYPE: protein
271     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
275 Met Ala Val Phe Glu Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly
276   1           5           10           15
279 Ser Gly Met Ile Gly Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu
280           20           25           30
283 Leu Gly Asp Val Val Leu Phe Asp Val Val Pro Asn Met Pro Met Gly
284           35           40           45
287 Lys Ala Met Asp Ile Ser His Asn Ser Ser Val Val Asp Thr Gly Ile
288           50           55           60
291 Thr Val Tyr Gly Ser Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val
292   65           70           75           80
295 Val Ile Ile Thr Ala Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys
296           85           90           95
299 Glu Trp Ser Arg Met Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg
300           100          105          110
303 Glu Val Gly Ala Ala Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile
304           115          120          125
308 Asn Ile Thr Asn Pro Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser
309           130          135          140
313 Ser Gly Leu Pro His His Arg Ile Cys Gly Met Ala Gly Met Leu Asp
314 145          150          155          160
318 Ser Ser Arg Phe Arg Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro
319           165          170          175
323 Arg Asp Val Gln Gly Met Val Ile Gly Val His Gly Asp His Met Val
324           180          185          190
328 Pro Leu Ser Arg Tyr Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe
329           195          200          205
333 Val Lys Lys Gly Trp Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln
334           210          215          220
338 Lys Thr Lys Val Ala Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly
339 225          230          235          240
343 Ser Ala Tyr Tyr Ala Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser
344           245          250          255
348 Tyr Leu Lys Asp Arg Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln
349           260          265          270
353 Gly Gln Tyr Gly Val Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile
354           275          280          285
357 Gly Gly Arg Gly Val Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln
358           290          295          300

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362	Glu	Arg	Gln	Glu	Leu	Gln	Gly	Ser	Ile	Asp	Glu	Val	Lys	Glu	Met	Gln
363	305				310					315						320
367	Lys	Ala	Ile	Ala	Ala	Leu	Asp	Ala	Ser	Lys						
368				325						330						

VERIFICATION SUMMARY

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L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]